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TO: EXAMINER MEDINA IBRAHIM; USPTO
FROM: GINNIE DRESS (virginia.dress@pioneer.com) *vmc*
RE: US APPLICATION 10/782,436; Atty Docket 1121D
DATE: October 13, 2005 FAX NUMBER: (571) 273-0797
NUMBER OF PAGES FOLLOWING THIS SHEET: 21

Examiner Ibrahim,

Attached please find the requested information comprising a summary of percent sequence identity and the alignments, as determined by GAP analyses, for SEQ ID NOS: 2, 4, 6, 8, and 10 from the above referenced application.

Other GAP analyses are available, for example, vs. Arabidopsis RuvB (Rvb1).

Sincerely,
Virginia Dress
Reg. 48,243

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If there is a problem with transmission or illegible pages, please contact the sender or (515) 270-4192.

Application 10/782,436

Applicant Docket Ref: 1121D

1121D RuvB

GAP comparison of sequences in application as originally filed.

Polynucleotides – Percent Sequence Identity

SEQ ID	3	5	7	9
1	97.556	88.091	89.659	97.236
3	100	87.166	89.117	97.247
5	---	100	99.282	87.081
7	---	---	100	89.109

Polypeptides – Percent Sequence Identity

SEQ ID	4	6	8	10
2	99.341	96.923	96.923	99.543
4	100	97.582	97.582	100
6	---	100	100	97.489
8	---	---	100	97.489

Individual pairwise GAP alignments of polypeptides on following pages.

*enablement - mod. by
reclaim
from*

10/782,436

1121D *571-273-
6797*

claim 5

allowable

*Summary GAP
alignments*

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RUVB
to: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RUVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2253	Length:	455
Ratio:	4.952	Gaps:	0
Percent Similarity:	99.560	Percent Identity:	99.341

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID4 November 5, 2001 17:08 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQSAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

51 LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

101 VYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTTCGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTTCGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

151 AKSISHVVIISLKT VKG TKQLKLDSS IYDALIKEKVAVGDV IY IEANS GAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AKSISHVVIISLKT VKG TKQLKLDSS IYDALIKEKVAVGDV IY IEANS GAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

201 KRVGRCD SFATEYDLEAE EYVPI PKGEV HKKKEIVQDVT LHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KRVGRCD SFATEYDLEAE EYVPI PKGEV HKKKEIVQDVT LHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

251 QGGQDILSLMGQMMKPRKTEITEKLRQSEINKVVNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 QGGQDILSLMGQMMKPRKTEITEKLRQSEINKVVNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

301 IDEVHMLDIECF SYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 IDEVHMLDIECF SYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||
351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDMDEESLAYLGBIGQQT 400
|||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
451 ERYIT 455
|||||
451 ERYIT 455

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuVB
to: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2212	Length:	455
Ratio:	4.862	Gaps:	0
Percent Similarity:	97.363	Percent Identity:	96.923

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID6 November 5, 2001 17:09 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAACFVGQSAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG 50

51 LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100

101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGEVTELSPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGEVIELSPEEAESTTGGY 150

151 AKSISHVVIISLKTIVKGTKQLKLDSSIYDALIKEKVAVGDVIYIEANS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AKSISHVVIIGLKTIVKGTKQLKLDPSIYDALIKEKVAVGDVIYIEANS 200

201 KRVGRCDSPATEYDLEAEEYVPIPKGEVHKKKEIVQDVTLHDLDAANA 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KRVGRCDSPATEYDLEAEEYVPIPKGEVHKKKEIVQDVTLHDLDAANA 250

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 300

301 IDEVHMLDIECFSYLNRALSPSPVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 IDEVHMLDIECFSYLNRALSPSPVILATNRGICNVRGTDMTSPHGIP 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||:|||||
351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDAKSSARLLQEQQ 450
|||||:|||||.|||||.|||||
401 SLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDAKSSARLLQEQQ 450
451 ERYIT 455
|||||
451 ERYIT 455

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuvB
to: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2202	Length:	456
Ratio:	4.840	Gaps:	1
Percent Similarity:	97.363	Percent Identity:	96.923

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID8

November 5, 2001 17:09 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVGQSAAREAA 49
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVGQAAAREAA 50

50 GLAVDMIRQKKMAGRAVLLVGPPATGKTALALCIAQELGSKVPFCPMVGS 99
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALCIAQELGSKVPFCPMVGS 100

100 EVYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVTELSPEEAESTTGG 149
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 EVYSSEVKKTEVLMENFRRAIGLRIKENKEVYEGEVIELSPPEEAESTTGG 150

150 YAKSISHVVIISLKTVMGTQQLKLDSSIIYDALIKEKVAVGDVYIEANSGA 199
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 YAKSISHVVIIGLKTVMGTQQLKLDPSIIYDALIKEKVAVGDVYIEANSGA 200

200 VKRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 249
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 VKRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250

250 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 299
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300

300 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 349
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

```
350 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQ 399
    |||||
351 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
    |||||
400 TSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQ 449
    |||||
401 TSLRHAIQLLSPASVVAKTNGREKMKADLEEVSGLYLDKSSARLLQEQ 450
    |||||
450 QERYIT 455
    |||||
451 QERYIT 456
```


Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID2 check: 9422 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 2 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2129	Length:	455
Ratio:	4.861	Gaps:	2
Percent Similarity:	99.772	Percent Identity:	99.543

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

1121SID2 x 1121SID10 November 5, 2001 17:10 ..

```
1 MRIBEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVGQSAAREAAC 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIBEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRAVLLVGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGSE 83

101 VYSSEVKKTEVLMENFRRRAICLRIKENKEVYEGEVTELSPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 VYSSEVKKTEVLMENFRRRAICLRIKENKEVYEGEVTELSPEEAESTTGGY 133

151 AKSISHVIIISLKTIVKGTQQLKLDSSIYDALIKEKVAVGDVIYIEANSGAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 AKSISHVIIISLKTIVKGTQQLKLDSSIYDALIKEKVAVGDVIYIEANSGAV 183

201 KRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
184 KRVGRCDSPATEYDLEABEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
234 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 283

301 IDEVHMLDIECFSYLNRALESPLSPVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
284 IDEVHMLDIECFSYLNRALESPLSPVILATNRGICNVRGTDMTSPHGIP 333
```

Application 10/782,436

Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEDIDMDEESLAYLGEIGQQT 400
|||||
334 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383
|||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
|||||
384 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 433
|||||
451 ERYIT 455
|||||
434 ERYIT 438

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2222	Length:	455
Ratio:	4.884	Gaps:	0
Percent Similarity:	97.802	Percent Identity:	97.582

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID4 x 1121SID6

November 5, 2001 17:11 ..

```
1 MRIBEVQSTSKQRIATHTHIKGLGLDANGMAIALAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIBEVQSTSKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG 50

51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAVDMIRQKKMAGRALLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100

101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAEESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 VYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAEESTTGGY 150

151 AKSISHVIIISLKTIVKGTQQLKLDSSIYDALIKEKVAVGCDVIYIEANS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AKSISHVIIIGLKTIVKGTQQLKLDPSIYDALIKEKVAVGCDVIYIEANS 200

201 KRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVLF 300

301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

```
351 VDLLDRLVIIRTETETGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 400
   |||||||
351 VDLLDRLVIIRTETETGPTMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
   |||||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
   |||||||
401 SLRHAIQLISPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQQ 450
   |||||||
451 ERYIT 455
   |||||
451 ERYIT 455
```

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuvB
Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003
Quality: 2212 Length: 456
Ratio: 4.862 Gaps: 1
Percent Similarity: 97.802 Percent Identity: 97.582

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

1121SID4 x 1121SID8

November 5, 2001 17:11 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVCQAAAREAA 49
|||||
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVCQAAAREAA 50
50 GLAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 99
|||||
51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 100
100 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETELSPPEAESTTGG 149
|||||
101 EVYSSEVKKTEVLMENFRAIGLRIKENKEVYEGETEIVLSPEEAESTTGG 150
150 YAKSISHVVIISLKTVMGKTKQLKLDSSIIDALIKEKVAVGQVVIYEANS 199
|||||
151 YAKSISHVVIISLKTVMGKTKQLKLDPSIIDALIKEKVAVGQVVIYEANS 200
200 VKRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 249
|||||
201 VKRVGRCDSFATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
250 PQGGQDILSLMCQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 299
|||||
251 PQGGQDILSLMCQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300
300 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 349
|||||
301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
```

Application 10/782,436

Applicant Docket Ref: 1121D

350 PVDLLDRLVIRTETYGPTTEMIQILAIRAQVEEIDMDEESLAYLGEIGQQ 399
|||||
351 PVDLLDRLVIRTETYGPTTEMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
|||||
400 TSLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQ 449
|||||
401 TSLRHAIQLLSPASVVAKTNGREKMKADLEEVSGLYLDKSSARLLQEQ 450
|||||
450 QERYIT 455
|||||
451 QERYIT 456

Application 10/782,436

Applicant Docket Ref: 1121D

GAP of: 1121SID4 check: 8436 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 4 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB
Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003
Quality: 2136 Length: 455
Ratio: 4.877 Gaps: 2
Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID4 x 1121SID10 November 5, 2001 17:11 ..

```
1 MRIEEVQSTSKKORIATHTHIKGLGLDANGMAIALAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRAVLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGSE 83

101 VYSSEVKKTEVLMENFRRALGLRIKENKEVYEGEVTELSPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 VYSSEVKKTEVLMENFRRALGLRIKENKEVYEGEVTELSPEEAESTTGGY 133

151 AKSISHVVIISLKTIVKGTKQLKLDSSIIYDALIKEKVAVGDVIYIEANGAV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 AKSISHVVIISLKTIVKGTKQLKLDSSIIYDALIKEKVAVGDVIYIEANGAV 183

201 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
184 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQP 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEIINKVNNRYIDEGIAELVPGVLF 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
234 QGGQDILSLMGQMMKPRKTEITEKLRQEIINKVNNRYIDEGIAELVPGVLF 283

301 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
284 IDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGIP 333
```

Application 10/782,436

Applicant Docket Ref: 1121D

```
351 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 400
    ||||||||||||||||||||||||||||||||||||||||||||
334 VDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383
    ||||||||||||||||||||||||||||||||||||||||||||
401 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 450
    ||||||||||||||||||||||||||||||||||||||||||||
384 SLRHAIQLISPASVVSKTNGREKICKADLEEVSGLYLDKSSARLLQEQQ 433
    ||||||
451 ERYIT 455
    |||||
434 ERYIT 438
```


Applicant Docket Ref: 1121D

PAGE 17/22 * RCVD AT 10/13/2005 12:14:34 PM [Eastern Daylight Time] * SVR:USPTO-EFXRF-6/26 * DNIS:2730797 * CSID:515 334 6883 * DURATION (mm:ss):05-02

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Applicant Docket Ref: 1121D

350 PVDLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDDESLAYLGEIGQQ 399
|||||
351 PVOLLDRLVIIRTETYGPTMIQILAIRAQVEEIDIDERSLAYLGEIGQQ 400
|||||
400 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQ 449
|||||
401 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDKSSARLLQEQ 450
|||||
450 QERYIT 455
|||||
451 QERYIT 456

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Applicant Docket Ref: 1121D

GAP of: 1121SID6 check: 8413 from: 1 to: 455
WPDEF Case 1121 SEQ ID NO: 6 RuvB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuvB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight: 8 Average Match: 2.912
Length Weight: 2 Average Mismatch: -2.003
Quality: 2095 Length: 455
Ratio: 4.783 Gaps: 2
Percent Similarity: 97.717 Percent Identity: 97.489

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

1121SID6 x 1121SID10 November 5, 2001 17:13 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMSMPLAAGFVGQAAAREAAAG 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MRIEEVQSTSKKQRIATHTHIKGLGLDANGMAIALAAGFVG..... 41

51 LAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGSE 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGSE 83

101 VYSSEVKKTEVLMENFRAICLRIVENKEVVEGEVIELSPPEEAESTTGGY 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
84 VYSSEVKKTEVLMENFRAICLRIVENKEVVEGEVTELSPEEAESTTGGY 133

151 AKSISHVIIIGLKTVMGKTKQLKLDPSIYDALIKEKVAVGDVIYIEANS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 AKSISHVIIISLKTVMGKTKQLKLDSSIYDALIKEKVAVGDVIYIEANS 183

201 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
184 KRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 233

251 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
234 QGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGV 283

301 IDEVHMLDIECFSYLNRALSPSPILATNRGICNVRGTDMTSPHGIP 350
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
284 IDEVHMLDIECFSYLNRALSPSPILATNRGICNVRGTDMTSPHGIP 333
```

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Applicant Docket Ref: 1121D

351 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDIDEESLAYLGEIGQQT 400
|||||
334 VDLLDRLVIIRTETYGPTTEMIQILAIRAQVEEIDMDEESLAYLGEIGQQT 383
401 SLRHAIQLLSPASVVAKTINGREKMCKADLEEVSGLYLDKSSARLLQEQQ 450
|||||:|||||
384 SLRHAIQLLSPASVVSKTINGREKICKADLEEVSGLYLDKSSARLLQEQQ 433
451 ERYIT 455
|||||
434 ERYIT 438

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Applicant Docket Ref: 1121D

GAP of: 1121SID8 check: 2111 from: 1 to: 456
WPDEF Case 1121 SEQ ID NO: 8 RuVB
to: 1121SID10 check: 7631 from: 1 to: 438
WPDEF Case 1121 SEQ ID NO: 10 RuVB

Symbol comparison table:
/app/gcg/10.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA
89: 10915-10919.

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	2085	Length:	456
Ratio:	4.760	Gaps:	3
Percent Similarity:	97.717	Percent Identity:	97.489

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1121SID8 x 1121SID10 November 5, 2001 17:14 ..

```
1 MRIEEVQSTSKKQRIATHTHIKGLGLDQANGMSMPLAAGFVGQAAAREAA 50
  |||||
1 MRIEEVQSTSKKQRIATHTHIKGLGLD.ANGMAIALAAGFVG..... 41

51 GLAVDMIRQKKMAGRALLLAGPPATGKTALALGIAQELGSKVPFCPMVGS 100
  |||||
42 .....QKKMAGRAVLLAGPPATGKTALA.GIAQELGSKVPFCPMVGS 82

101 EVYSSEVKKTEVLMENFRRRAIGLRIKENKEVYEGEVIELSPPEAESTTGG 150
  |||||
83 EVYSSEVKKTEVLMENFRRRAIGLRIKENKEVYEGEVTELSPEAESTTGG 132

151 YAKSISHVIGLTKTVKGTKQLKLDPSIYDALIKEKVAVGDVIYIEANSGA 200
  |||||
133 YAKSISHVVISLTKTVKGTKQLKLDSSIYDALIKEKVAVGDVIYIEANSGA 182

201 VKRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 250
  |||||
183 VKRVGRCDSPATEYDLEAEYVPIPKGEVHKKKEIVQDVTLHDLDAANAQ 232

251 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 300
  |||||
233 PQGGQDILSLMGQMMKPRKTEITEKLRQEINKVVNRYIDEGIAELVPGVL 282

301 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 350
  |||||
283 FIDEVHMLDIECFSYLNRALESPLSPIVILATNRGICNVRGTDMTSPHGI 332
```

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Applicant Docket Ref: 1121D

351 PVDLLDRLVIRRTETYGPTETMIQILAIRAQVEEIDIDEESLAYLGEIGQQ 400
|||||
333 PVDLLDRLVIRRTETYGPTETMIQILAIRAQVEEIDMDDEESLAYLGEIGQQ 382
401 TSLRHAIQLLSPASVVAKTNGREKMCKADLEEVSGLYLDAKSSARLLQEQ 450
|||||:|||||.|||||.|||||
383 TSLRHAIQLLSPASVVSKTNGREKICKADLEEVSGLYLDAKSSARLLQEQ 432
451 QERYIT 456
|||||
433 QERYIT 438